

SEQUENCE LISTING

<110> Cihlar, Tomas

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PC

<140> unassigned

<141> 1999-06-10

<150> 60/088,864

<151> 1998-06-11

<150> 60/132,267

<151> 1999-05-03

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<170> PatentIn Ver. 2.0

<210> 1

<211> 2123

<212> DNA

<213> Unknown

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<223> Description of Unknown Organism: This information
 is not available.

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<221> CDS

<222> (263)..(1912)

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ggactcagct cccgggaagc aaccagctg cggaggcaac ggcagtgtg ctcctccagc 180

gaaggacagc aggcaggcag acagacagag gtctggggac tggaaggcct cagccccag 240

ccactgggct gggcctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292

Met Ala Phe Asn Asp Leu Leu Gln Gln Val
 1 5 10

ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc ctc 340

Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu
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ccc	ctg	ctc	ctg	atg	gct	tct	cac	aac	acc	ctg	cag	aac	ttc	act	gct	388
Pro	Leu	Leu	Leu	Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala	
			30					35					40			
gcc	atc	cct	acc	cac	cac	tgc	cgc	ccg	cct	gcc	gat	gcc	aac	ctc	agc	436
Ala	Ile	Pro	Thr	His	His	Cys	Arg	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser	
		45					50					55				
aag	aac	ggg	ggg	ctg	gag	gtc	tgg	ctg	ccc	cgg	gac	agg	cag	ggg	cag	484
Lys	Asn	Gly	Gly	Leu	Glu	Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln	
	60					65					70					
cct	gag	tcc	tgc	ctc	cgc	ttc	acc	tcc	ccg	cag	tgg	gga	ctg	ccc	ttt	532
Pro	Glu	Ser	Cys	Leu	Arg	Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe	
	75				80					85					90	
ctc	aat	ggc	aca	gaa	gcc	aat	ggc	aca	ggg	gcc	aca	gag	ccc	tgc	acc	580
Leu	Asn	Gly	Thr	Glu	Ala	Asn	Gly	Thr	Gly	Ala	Thr	Glu	Pro	Cys	Thr	
				95					100					105		
gat	ggc	tgg	atc	tat	gac	aac	agc	acc	ttc	cca	tct	acc	atc	gtg	act	628
Asp	Gly	Trp	Ile	Tyr	Asp	Asn	Ser	Thr	Phe	Pro	Ser	Thr	Ile	Val	Thr	
			110					115					120			
gag	tgg	gac	ctt	gtg	tgc	tct	cac	agg	gcc	cta	cgc	cag	ctg	gcc	cag	676
Glu	Trp	Asp	Leu	Val	Cys	Ser	His	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln	
		125					130					135				
tcc	ttg	tac	atg	gtg	ggg	gtg	ctg	ctc	gga	gcc	atg	gtg	ttc	ggc	tac	724
Ser	Leu	Tyr	Met	Val	Gly	Val	Leu	Leu	Gly	Ala	Met	Val	Phe	Gly	Tyr	
	140					145					150					
ctt	gca	gac	agg	cta	ggc	cgc	cgg	aag	gta	ctc	atc	ttg	aac	tac	ctg	772
Leu	Ala	Asp	Arg	Leu	Gly	Arg	Arg	Lys	Val	Leu	Ile	Leu	Asn	Tyr	Leu	
	155				160					165					170	
cag	aca	gct	gtg	tca	ggg	acc	tgc	gca	gcc	ttc	gca	ccc	aac	ttc	ccc	820
Gln	Thr	Ala	Val	Ser	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Asn	Phe	Pro	
				175				180						185		
atc	tac	tgc	gcc	ttc	cgg	ctc	ctc	tgc	ggc	atg	gct	ctg	gct	ggc	atc	868
Ile	Tyr	Cys	Ala	Phe	Arg	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Gly	Ile	
			190					195					200			
tcc	ctc	aac	tgc	atg	aca	ctg	aat	gtg	gag	tgg	atg	ccc	att	cac	aca	916
Ser	Leu	Asn	Cys	Met	Thr	Leu	Asn	Val	Glu	Trp	Met	Pro	Ile	His	Thr	
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cgg	gcc	tgc	gtg	ggc	acc	ttg	att	ggc	tat	gtc	tac	agc	ctg	ggc	cag	964
Arg	Ala	Cys	Val	Gly	Thr	Leu	Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln	
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ttc	ctc	ctg	gct	ggg	gtg	gcc	tac	gct	gtg	ccc	cac	tgg	cgc	cac	ctg	1012
Phe	Leu	Leu	Ala	Gly	Val	Ala	Tyr	Ala	Val	Pro	His	Trp	Arg	His	Leu	
235					240					245					250	
cag	cta	ctg	gtc	tct	gcg	cct	ttt	ttt	gcc	ttc	ttc	atc	tac	tcc	tgg	1060
Gln	Leu	Leu	Val	Ser	Ala	Pro	Phe	Phe	Ala	Phe	Phe	Ile	Tyr	Ser	Trp	
				255					260					265		
ttc	ttc	att	gag	tcg	gcc	cgc	tgg	cac	tcc	tcc	tcc	ggg	agg	ctg	gac	1108
Phe	Phe	Ile	Glu	Ser	Ala	Arg	Trp	His	Ser	Ser	Ser	Gly	Arg	Leu	Asp	
			270					275					280			
ctc	acc	ctg	agg	gcc	ctg	cag	aga	gtc	gcc	cgg	atc	aat	ggg	aag	cgg	1156
Leu	Thr	Leu	Arg	Ala	Leu	Gln	Arg	Val	Ala	Arg	Ile	Asn	Gly	Lys	Arg	
			285				290					295				
gaa	gaa	gga	gcc	aaa	ttg	agt	atg	gag	gta	ctc	cgg	gcc	agt	ctg	cag	1204
Glu	Glu	Gly	Ala	Lys	Leu	Ser	Met	Glu	Val	Leu	Arg	Ala	Ser	Leu	Gln	
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aag	gag	ctg	acc	atg	ggc	aaa	ggc	cag	gca	tcg	gcc	atg	gag	ctg	ctg	1252
Lys	Glu	Leu	Thr	Met	Gly	Lys	Gly	Gln	Ala	Ser	Ala	Met	Glu	Leu	Leu	
315					320					325					330	
cgc	tgc	ccc	acc	ctc	cgc	cac	ctc	ttc	ctc	tgc	ctc	tcc	atg	ctg	tgg	1300
Arg	Cys	Pro	Thr	Leu	Arg	His	Leu	Phe	Leu	Cys	Leu	Ser	Met	Leu	Trp	
				335				340						345		
ttt	gcc	act	agc	ttt	gca	tac	tat	ggg	ctg	gtc	atg	gac	ctg	cag	ggc	1348
Phe	Ala	Thr	Ser	Phe	Ala	Tyr	Tyr	Gly	Leu	Val	Met	Asp	Leu	Gln	Gly	
			350					355					360			
ttt	gga	gtc	agc	atc	tac	cta	atc	cag	gtg	atc	ttt	ggg	gct	gtg	gac	1396
Phe	Gly	Val	Ser	Ile	Tyr	Leu	Ile	Gln	Val	Ile	Phe	Gly	Ala	Val	Asp	
		365				370						375				
ctg	cct	gcc	aag	ctt	gtg	ggc	ttc	ctt	gtc	atc	aac	tcc	ctg	ggg	cgc	1444
Leu	Pro	Ala	Lys	Leu	Val	Gly	Phe	Leu	Val	Ile	Asn	Ser	Leu	Gly	Arg	
	380					385					390					
cgg	cct	gcc	cag	atg	gct	gca	ctg	ctg	ctg	gca	ggc	atc	tgc	atc	ctg	1492
Arg	Pro	Ala	Gln	Met	Ala	Ala	Leu	Leu	Leu	Ala	Gly	Ile	Cys	Ile	Leu	
395					400					405					410	
ctc	aat	ggg	gtg	ata	ccc	cag	gac	cag	tcc	att	gtc	cga	acc	tct	ctt	1540
Leu	Asn	Gly	Val	Ile	Pro	Gln	Asp	Gln	Ser	Ile	Val	Arg	Thr	Ser	Leu	
				415				420						425		
gct	gtg	ctg	ggg	aag	ggg	tgt	ctg	gct	gcc	tcc	ttc	aac	tgc	atc	ttc	1588
Ala	Val	Leu	Gly	Lys	Gly	Cys	Leu	Ala	Ala	Ser	Phe	Asn	Cys	Ile	Phe	
			430					435					440			

ctg	tat	act	ggg	gaa	ctg	tat	ccc	aca	atg	atc	cgg	cag	aca	ggc	atg	1636
Leu	Tyr	Thr	Gly	Glu	Leu	Tyr	Pro	Thr	Met	Ile	Arg	Gln	Thr	Gly	Met	
		445					450					455				
gga	atg	ggc	agc	acc	atg	gcc	cga	gtg	ggc	agc	atc	gtg	agc	cca	ctg	1684
Gly	Met	Gly	Ser	Thr	Met	Ala	Arg	Val	Gly	Ser	Ile	Val	Ser	Pro	Leu	
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gtg	agc	atg	act	gcc	gag	ctc	tac	ccc	tcc	atg	cct	ctc	ttc	atc	tac	1732
Val	Ser	Met	Thr	Ala	Glu	Leu	Tyr	Pro	Ser	Met	Pro	Leu	Phe	Ile	Tyr	
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ggt	gct	gtt	cct	gtg	gcc	gcc	agc	gct	gtc	act	gtc	ctc	ctg	cca	gag	1780
Gly	Ala	Val	Pro	Val	Ala	Ala	Ser	Ala	Val	Thr	Val	Leu	Leu	Pro	Glu	
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acc	ctg	ggc	cag	cca	ctg	cca	gac	acg	gtg	cag	gac	ctg	gag	agc	agg	1828
Thr	Leu	Gly	Gln	Pro	Leu	Pro	Asp	Thr	Val	Gln	Asp	Leu	Glu	Ser	Arg	
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aaa	ggg	aaa	cag	acg	cga	cag	caa	caa	gag	cac	cag	aag	tat	atg	gtc	1876
Lys	Gly	Lys	Gln	Thr	Arg	Gln	Gln	Gln	Glu	His	Gln	Lys	Tyr	Met	Val	
		525					530					535				
cca	ctg	cag	gcc	tca	gca	caa	gag	aag	aat	gga	ctc	tgaggactga				1922
Pro	Leu	Gln	Ala	Ser	Ala	Gln	Glu	Lys	Asn	Gly	Leu					
	540					545					550					
gaaggggcct	tacagaaccc	taaagggagg	gaaggtccta	caggtctccg	gccacccaca											1982
caaggaggag	gaagaggaaa	tggtgaccca	agtgtggggg	ttgtggttca	ggaaagcatc											2042
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 Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
 35 40 45

Cys Arg Pro Pro Ala Asp Ala Asn Leu Ser Lys Asn Gly Gly Leu Glu
 50 55 60
 Val Trp Leu Pro Arg Asp Arg Gln Gly Gln Pro Glu Ser Cys Leu Arg
 65 70 75 80
 Phe Thr Ser Pro Gln Trp Gly Leu Pro Phe Leu Asn Gly Thr Glu Ala
 85 90 95
 Asn Gly Thr Gly Ala Thr Glu Pro Cys Thr Asp Gly Trp Ile Tyr Asp
 100 105 110
 Asn Ser Thr Phe Pro Ser Thr Ile Val Thr Glu Trp Asp Leu Val Cys
 115 120 125
 Ser His Arg Ala Leu Arg Gln Leu Ala Gln Ser Leu Tyr Met Val Gly
 130 135 140
 Val Leu Leu Gly Ala Met Val Phe Gly Tyr Leu Ala Asp Arg Leu Gly
 145 150 155 160
 Arg Arg Lys Val Leu Ile Leu Asn Tyr Leu Gln Thr Ala Val Ser Gly
 165 170 175
 Thr Cys Ala Ala Phe Ala Pro Asn Phe Pro Ile Tyr Cys Ala Phe Arg
 180 185 190
 Leu Leu Ser Gly Met Ala Leu Ala Gly Ile Ser Leu Asn Cys Met Thr
 195 200 205
 Leu Asn Val Glu Trp Met Pro Ile His Thr Arg Ala Cys Val Gly Thr
 210 215 220
 Leu Ile Gly Tyr Val Tyr Ser Leu Gly Gln Phe Leu Leu Ala Gly Val
 225 230 235 240
 Ala Tyr Ala Val Pro His Trp Arg His Leu Gln Leu Leu Val Ser Ala
 245 250 255
 Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp Phe Phe Ile Glu Ser Ala
 260 265 270
 Arg Trp His Ser Ser Ser Gly Arg Leu Asp Leu Thr Leu Arg Ala Leu
 275 280 285
 Gln Arg Val Ala Arg Ile Asn Gly Lys Arg Glu Glu Gly Ala Lys Leu
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<223> Description of Unknown Organism: This information
is not available.

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